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PCT09

RAW SEQUENCE LISTING

DATE: 12/21/2001

PATENT APPLICATION: US/09/720,583A

TIME: 13:24:11

Input Set : A:\MBHB00-1314 SequenceListing.txt

Output Set: N:\CRF3\12212001\I720583A.raw

ENTERED

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3 <110> APPLICANT: DSM N.V.
4     POUWELS, Pieter
5     van LUIJK, Nicole
6     JORE, Johannes
7     LUITEN, Rudolf
9 <120> TITLE OF INVENTION: Propionibacterium Vector
11 <130> FILE REFERENCE: MBHB00-1314
13 <140> CURRENT APPLICATION NUMBER: US 09/720,583A
14 <141> CURRENT FILING DATE: 2000-12-22
16 <150> PRIOR APPLICATION NUMBER: PCT/EP99/04416
17 <151> PRIOR FILING DATE: 1999-06-25
19 <150> PRIOR APPLICATION NUMBER: EP 98305033.7
20 <151> PRIOR FILING DATE: 1998-06-25
22 <160> NUMBER OF SEQ ID NOS: 13
24 <170> SOFTWARE: PatentIn version 3.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 3555
28 <212> TYPE: DNA
29 <213> ORGANISM: Propionibacterium freudenreichii LMG16545
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (273)..(1184)
36 <400> SEQUENCE: 1
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39 gccgcaatgc ccgaacacgc cccagccatc ccttgagca ggtggcagcg tcaggggagt 120
41 cgggggatgt ttggcagggg atgtggaaag agagttcgct ttgctcacat ggctcaaccg 180
43 ggtaactaac tgatatgggg tcttcgtcgc ccactttgaa cagccgagg aatggaccac 240
45 gctgaacgtg actcgcatgc ttcactgcat gt atg gat tcg ttc gag acg ttg 293
46                                     Met Asp Ser Phe Glu Thr Leu
47                                     1             5
49 ttc cct gag agc tgg ctg cca cgc aag ccg ctg gcg tca gcc gag aag 341
50 Phe Pro Glu Ser Trp Leu Pro Arg Lys Pro Leu Ala Ser Ala Glu Lys
51     10             15             20
53 tct ggg gcg tac cgg cac gtg act cgg cag agg gcg ctg gag ctg cct 389
54 Ser Gly Ala Tyr Arg His Val Thr Arg Gln Arg Ala Leu Glu Leu Pro
55     25             30             35
57 tac atc gaa gcg aac ccg ttg gtc atg cag tcc ttg gtc atc acc gat 437
58 Tyr Ile Glu Ala Asn Pro Leu Val Met Gln Ser Leu Val Ile Thr Asp
59 40             45             50             55
61 cga gat gct tcg gat gct gac tgg gcc gca gac ctc gct ggg ctg cct 485
62 Arg Asp Ala Ser Asp Ala Asp Trp Ala Ala Asp Leu Ala Gly Leu Pro
63     60             65             70
65 tca ccg tcc tac gtg tcc atg aac cgt gtc acg acc acc gga cac atc 533
66 Ser Pro Ser Tyr Val Ser Met Asn Arg Val Thr Thr Thr Gly His Ile
67     75             80             85
69 gtc tat gcc ttg aag aac cct gtg tgt ctg acc gat gcc gcg cgg cga 581
70 Val Tyr Ala Leu Lys Asn Pro Val Cys Leu Thr Asp Ala Ala Arg Arg

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71          90          95          100
73 cgg cct atc aac ctg ctc gcc cgc gtc gag cag ggc cta tgc gac gtt 629
74 Arg Pro Ile Asn Leu Leu Ala Arg Val Glu Gln Gly Leu Cys Asp Val
75      105      110      115
77 ctc ggc ggc gat gca tcc tac ggg cac cgg atc aca aag aac ccg ctc 677
78 Leu Gly Gly Asp Ala Ser Tyr Gly His Arg Ile Thr Lys Asn Pro Leu
79 120      125      130      135
81 agc acc gcc cat gcg acc ctc tgg ggc ccc gca gac gcg ctc tac gag 725
82 Ser Thr Ala His Ala Thr Leu Trp Gly Pro Ala Asp Ala Leu Tyr Glu
83      140      145      150
85 ctg cgc gcc ctc gca cac acc ctc gac gag atc cac gca ctg ccg gag 773
86 Leu Arg Ala Leu Ala His Thr Leu Asp Glu Ile His Ala Leu Pro Glu
87      155      160      165
89 gca ggg aac ccg cgt cgc aac gtc acc cga tca acg gtc ggc cgc aac 821
90 Ala Gly Asn Pro Arg Arg Asn Val Thr Arg Ser Thr Val Gly Arg Asn
91      170      175      180
93 gtc acc ctg ttc gac acc acc cgc atg tgg gca tac cgg gcc gtc cgg 869
94 Val Thr Leu Phe Asp Thr Thr Arg Met Trp Ala Tyr Arg Ala Val Arg
95      185      190      195
97 cac tcc tgg ggc ggc ccg gtc gcc gaa tgg gag cac acc gta ttc gag 917
98 His Ser Trp Gly Gly Pro Val Ala Glu Trp Glu His Thr Val Phe Glu
99 200      205      210      215
101 cac atc cac cta ctg aac gag acg atc atc gcc gac gaa ttc gcc aca 965
102 His Ile His Leu Leu Asn Glu Thr Ile Ile Ala Asp Glu Phe Ala Thr
103      220      225      230
105 ggc ccc ctc ggc ttg aac gaa ctt aag cac tta tot cga tcc att tcc 1013
106 Gly Pro Leu Gly Leu Asn Glu Leu Lys His Leu Ser Arg Ser Ile Ser
107      235      240      245
109 cga tgg gtc tgg cgc aac ttc acc ccc gaa acc ttc cgc gca cgc cag 1061
110 Arg Trp Val Trp Arg Asn Phe Thr Pro Glu Thr Phe Arg Ala Arg Gln
111      250      255      260
113 aaa gcg atc agc ctc cgt gga gca tcc aaa ggc ggc aaa gaa ggc ggc 1109
114 Lys Ala Ile Ser Leu Arg Gly Ala Ser Lys Gly Gly Lys Glu Gly Gly
115      265      270      275
117 cac aaa ggc ggc att gcc agt ggc gca tca cgg cgc gcc cat acc cgt 1157
118 His Lys Gly Gly Ile Ala Ser Gly Ala Ser Arg Arg Ala His Thr Arg
119 280      285      290      295
121 caa cag ttc ttg gag ggt ctc tca tga ccacacgtga acgtctcccc 1204
122 Gln Gln Phe Leu Glu Gly Leu Ser
123      300
125 cgcaacggct acagcatcgc cgtcgtcgcg aaaaagctcg gtgtctccga gtccaccgtc 1264
127 aagcgggtgga cttccgagcc acgcgaggag ttcgtggccc gcgttgccgc acgccacgcg 1324
129 cggattcgtg agctccgctc ggagggtcag agcatgcgtg cgattgctgc cgagggtcggg 1384
131 gtttccgtgg gcaccgtgca ctacgcgtg aacaagaatc gaactgacgc atgaccgtaa 1444
133 cgccgcacga tgagcatttt cttgatcgtg caccgcttgg cactacgttc gcgtgcgggtt 1504
135 gcacagtgcg cgccacgttc ttatcctgcg gccattgtgg ctacagccaa tggggggcat 1564
137 cagcaacgga cgttgaacct ggtgggcaag tgttactcag ggggacatgc ccagtctgcg 1624
139 gcgctcggat tgacggtatg gcagtcgtgc atgcggcccc accgtcaaac tcattcaggt 1684
141 atcagtgaga accctcatgg caccctctcg tgacacgttc tcgttgcgat cagctgctgt 1744

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143 gcgtgcgggc gtgagcgttt ctacgctgcg gcgcaggaaa tcagagcttg aggctgccgg 1804
145 agcgacggta gacccgtccg gttgggtggt gccactgcgt gcaactcaagg tcgttttttg 1864
147 ggtgtcagat gagacctoga atgcgcccgg tcatgacgct gagttagtgg cgcagctgcg 1924
149 ctctgagaac gagtttttac ggcgtcaggt cgagcagcag gcgcgcacga tcgaacggca 1984
151 ggctgaggca cacgcggttg tctcagcgca gctcacacgg gttggccagc ttgaggccgg 2044
153 cgacgcagca gcaccgacac tggcaccctg tgaaaggccg gctccgcgac ggcggtggtg 2104
155 gcagcgctcg tagcggctcag gatcgctctg gcgtgacgag tgtgtctggc agtgcgaaaca 2164
157 gttgctcgac cagtggcagc agaagcgaga tcgctgcgtg gtgctgttcc tcggtcagtt 2224
159 cgtcgaggac tggcgggtct tgctgcgtcc agccgatcgc ctccggcgcc aaggtcagtt 2284
161 ccaagctgtg ccaacgcaca cgcccctcgg ctgacagctg agtctcgaac tgtgcaactg 2344
163 gaccggccgg aagatgcacg ttgccgaggt cgtgagtggc caagcgacg tcaaagagtg 2404
165 ctgcttcgta gccgcgcaga aatggcagtg ctccgtcgat tcggatcggc ctgcccagggt 2464
167 acattccggg ccgcttgatg aacgcctccg cgtagaagcg caccgttctc ggcccggcct 2524
169 cgtgatctgt cactgtgcac gctcctctcg atggttctcg acgctaccgg agaccaccga 2584
171 cgttcatgcc cagcgcagcg acctgaaaagg accaagccga gttagccgtg ctaaccgtat 2644
173 agcttgctcc gtgcctctg agggcaacca cctgcgcagc aggtgggagg cagcccgcgc 2704
175 gcaagcgccct accgggtttg ggcaacagccc ataaatcaac gcctccggtg ttgaagcgat 2764
177 cgtgtgtcac gattgctatg cttgctaccc cttcagggtt ttctataca caaatcaagt 2824
179 tttttcgtat acgctaattg catgagttag catctactgc acggcaagcc cgtcaccaac 2884
181 gagcagattc aggcattggg agacgaggcc gaggccggat acgacctgcc caaactcccc 2944
183 aagccaaggc gcggacgccc gcccgtagga gacggtccgg gcaccgtcgt acccgtgcgt 3004
185 ctgcagcgcg ccaccgttgc cgctctcaca gaacgagcaa cagccgaggg catcacgaac 3064
187 cgttcagacg cgatccgagc cgcagtcacc gagtggacac ggggttgctg acctccacga 3124
189 ctcagcacgc aagcactacc aacgagaccg gctcgacgac acggccgtgc tctacgcggc 3184
191 caccacggtt ctcaactccc ggccactcga cgacgaagac gaccgcgcgc gctggctcat 3244
193 gatcggaacc gaccagcag gccgcctact cgaactcgtc gcaactgatc acgacgacgg 3304
195 ctacgaactg atcatccacg caatgaaagc ccgcacccaa tacctcgacc agctctaacc 3364
197 aagaaaggaa cctgatgagc gaccagctag acagcgaccg caactacgac ccgatgatct 3424
199 tcgacgtgat gcgcgagacc gcgaaccgcg tcgtcgccac gtacgttgca tgggaagatg 3484
201 aagccgctga tccccgcgag gctgcgcact ggcaggccga gcgattccgc acccggcacg 3544
203 aggtgcgcgc c 3555

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206 <210> SEQ ID NO: 2

207 <211> LENGTH: 303

208 <212> TYPE: PRT

209 <213> ORGANISM: Propionibacterium freudenreichii LMG16545

211 <400> SEQUENCE: 2

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212 Met Asp Ser Phe Glu Thr Leu Phe Pro Glu Ser Trp Leu Pro Arg Lys
213 1 5 10 15
215 Pro Leu Ala Ser Ala Glu Lys Ser Gly Ala Tyr Arg His Val Thr Arg
216 20 25 30
218 Gln Arg Ala Leu Glu Leu Pro Tyr Ile Glu Ala Asn Pro Leu Val Met
219 35 40 45
221 Gln Ser Leu Val Ile Thr Asp Arg Asp Ala Ser Asp Ala Asp Trp Ala
222 50 55 60
224 Ala Asp Leu Ala Gly Leu Pro Ser Pro Ser Tyr Val Ser Met Asn Arg
225 65 70 75 80
227 Val Thr Thr Thr Gly His Ile Val Tyr Ala Leu Lys Asn Pro Val Cys
228 85 90 95
230 Leu Thr Asp Ala Ala Arg Arg Arg Pro Ile Asn Leu Leu Ala Arg Val

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231          100          105          110
233 Glu Gln Gly Leu Cys Asp Val Leu Gly Gly Asp Ala Ser Tyr Gly His
234          115          120          125
236 Arg Ile Thr Lys Asn Pro Leu Ser Thr Ala His Ala Thr Leu Trp Gly
237          130          135          140
239 Pro Ala Asp Ala Leu Tyr Glu Leu Arg Ala Leu Ala His Thr Leu Asp
240 145          150          155          160
242 Glu Ile His Ala Leu Pro Glu Ala Gly Asn Pro Arg Arg Asn Val Thr
243          165          170          175
245 Arg Ser Thr Val Gly Arg Asn Val Thr Leu Phe Asp Thr Thr Arg Met
246          180          185          190
248 Trp Ala Tyr Arg Ala Val Arg His Ser Trp Gly Gly Pro Val Ala Glu
249          195          200          205
251 Trp Glu His Thr Val Phe Glu His Ile His Leu Leu Asn Glu Thr Ile
252          210          215          220
254 Ile Ala Asp Glu Phe Ala Thr Gly Pro Leu Gly Leu Asn Glu Leu Lys
255 225          230          235          240
257 His Leu Ser Arg Ser Ile Ser Arg Trp Val Trp Arg Asn Phe Thr Pro
258          245          250          255
260 Glu Thr Phe Arg Ala Arg Gln Lys Ala Ile Ser Leu Arg Gly Ala Ser
261          260          265          270
263 Lys Gly Gly Lys Glu Gly Gly His Lys Gly Gly Ile Ala Ser Gly Ala
264          275          280          285
266 Ser Arg Arg Ala His Thr Arg Gln Gln Phe Leu Glu Gly Leu Ser
267          290          295          300

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270 <210> SEQ ID NO: 3

271 <211> LENGTH: 85

272 <212> TYPE: PRT

273 <213> ORGANISM: Propionibacterium freudenreichii LMG16545

275 <400> SEQUENCE: 3

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276 Met Thr Thr Arg Glu Arg Leu Pro Arg Asn Gly Tyr Ser Ile Ala Ala
277 1          5          10          15
279 Ala Ala Lys Lys Leu Gly Val Ser Glu Ser Thr Val Lys Arg Trp Thr
280          20          25          30
282 Ser Glu Pro Arg Glu Glu Phe Val Ala Arg Val Ala Ala Arg His Ala
283          35          40          45
285 Arg Ile Arg Glu Leu Arg Ser Glu Gly Gln Ser Met Arg Ala Ile Ala
286          50          55          60
288 Ala Glu Val Gly Val Ser Val Gly Thr Val His Tyr Ala Leu Asn Lys
289 65          70          75          80

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291 Asn Arg Thr Asp Ala

292 85

295 <210> SEQ ID NO: 4

296 <211> LENGTH: 59

297 <212> TYPE: DNA

298 <213> ORGANISM: Artificial Sequence

300 <220> FEATURE:

301 <223> OTHER INFORMATION: Synthetic Duplex DNA designed to link EcoRI and AvaI

303 <400> SEQUENCE: 4

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304 aattcaagct tgtcgacgtt aacctgcagg catgcggatc cggtagcgat atcagatct 59
307 <210> SEQ ID NO: 5
308 <211> LENGTH: 59
309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial Sequence
312 <220> FEATURE:
313 <223> OTHER INFORMATION: Synthetic Duplex DNA designed to link EcoRI and AvaI
315 <400> SEQUENCE: 5
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319 <210> SEQ ID NO: 6
320 <211> LENGTH: 24
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial Sequence
324 <220> FEATURE:
325 <223> OTHER INFORMATION: Synthetic DNA designed to create Acc65I and BglII ends
327 <400> SEQUENCE: 6
328 gtaccggccg ctgcggccaa gctt 24
331 <210> SEQ ID NO: 7
332 <211> LENGTH: 24
333 <212> TYPE: DNA
334 <213> ORGANISM: Artificial Sequence
336 <220> FEATURE:
337 <223> OTHER INFORMATION: Synthetic DNA designed to create Acc65I and BglII ends
339 <400> SEQUENCE: 7
340 gatcaagctt ggccgcagcg gccg 24
343 <210> SEQ ID NO: 8
344 <211> LENGTH: 35
345 <212> TYPE: DNA
346 <213> ORGANISM: Artificial Sequence
348 <220> FEATURE:
349 <223> OTHER INFORMATION: Synthetic primer for erythromycin resistance
351 <400> SEQUENCE: 8
352 aaactgcagc tgctggcttg cgcccgatgc tagtc 35.
355 <210> SEQ ID NO: 9
356 <211> LENGTH: 76
357 <212> TYPE: DNA
358 <213> ORGANISM: Artificial Sequence
360 <220> FEATURE:
361 <223> OTHER INFORMATION: Synthetic primer for erythromycin resistance
363 <400> SEQUENCE: 9
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366 tgccgatacct ggttgc 76
369 <210> SEQ ID NO: 10
370 <211> LENGTH: 32
371 <212> TYPE: DNA
372 <213> ORGANISM: Artificial Sequence
374 <220> FEATURE:
375 <223> OTHER INFORMATION: Synthetic primer for cobA
377 <400> SEQUENCE: 10

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VERIFICATION SUMMARY

DATE: 12/21/2001

PATENT APPLICATION: US/09/720,583A

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